

SEQUENCE LISTING

<110> Rosanne M. Crooke
Mark J. Graham

<120> ANTISENSE MODULATION OF MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN
EXPRESSION

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<223> Antisense Oligonucleotide

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<213> Homo sapiens

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<221> CDS

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Met Ile Leu Leu Ala Val Leu Phe Leu

1

5

tgc ttc att tcc tca tat tca gct tct gtt aaa ggt cac aca act ggt 161
Glu Phe Ile Ser Ser Thr Ser Ala Ser Val Lys Gly His Thr Thr Gly

ctc tca tta aat aat gac cgg ctg tac aag ctc acg tac tcc act gaa	209
Leu Ser Leu Asn Asn Asp Arg Leu Tyr Lys Leu Thr Tyr Ser Thr Glu	
30 35 40	
ggt ctt ctt gat cgg ggc aaa gga aaa ctg caa gac agc gtg ggc tac	257
Val Leu Leu Asp Arg Gly Lys Gly Lys Leu Gln Asp Ser Val Gly Tyr	
45 50 55	
cgc att tcc tcc aac gtg gat gtg gcc tta cta tgg agg aat cct gat	305
Arg Ile Ser Ser Asn Val Asp Val Ala Leu Leu Trp Arg Asn Pro Asp	
60 65 70	
ggt gat gat gac cag ttg atc caa ata acg atg aag gat gta aat gtt	353
Gly Asp Asp Asp Gln Leu Ile Gln Ile Thr Met Lys Asp Val Asn Val	
75 80 85	
gaa aat gtg aat cag cag aga gga gag aag agc atc ttc aaa gga aaa	401
Glu Asn Val Asn Gln Gln Arg Gly Glu Lys Ser Ile Phe Lys Gly Lys	
90 95 100 105	
agc cca tct aaa ata atg gga aag gaa aac ttg gaa gct ctg caa aga	449
Ser Pro Ser Lys Ile Met Gly Lys Glu Asn Leu Glu Ala Leu Gln Arg	
110 115 120	
cct acg ctc ctt cat cta atc cat gga aag gtc aaa gag ttc tac tca	497
Pro Thr Leu Leu His Leu Ile His Gly Lys Val Lys Glu Phe Tyr Ser	
125 130 135	
tat caa aat gag gca gtg gcc ata gaa aat atc aag aga ggt ctg gct	545
Tyr Gln Asn Glu Ala Val Ala Ile Glu Asn Ile Lys Arg Gly Leu Ala	
140 145 150	
agc cta ttt cag aca cag tta agc tct gga acc acc aat gag gta gat	593
Ser Leu Phe Gln Thr Gln Leu Ser Ser Gly Thr Thr Asn Glu Val Asp	
155 160 165	
atc tct gga aat tgt aaa gtg acc tac cag gct cat caa gac aaa gtg	641
Ile Ser Gly Asn Cys Lys Val Thr Tyr Gln Ala His Gln Asp Lys Val	
170 175 180 185	
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Ile Lys Ile Lys Ala Leu Asp Ser Cys Lys Ile Ala Arg Ser Gly Phe	
190 195 200	
acg acc cca aat cag gtc ttg ggt gtc agt tca aaa gct aca tct gtc	737
Thr Thr Pro Asn Gln Val Leu Gly Val Ser Ser Lys Ala Thr Ser Val	
205 210 215	
acc acc tat aag ata gaa gac agc ttt gtt ata gct gtg ctt gct gaa	785
Thr Thr Tyr Lys Ile Glu Asp Ser Phe Val Ile Ala Val Leu Ala Glu	
220 225 230	
gaa aca cac aat ttt gga ctg aat ttc cta caa acc att aag ggg aaa	833
Glu Thr His Asn Phe Gly Leu Asn Phe Leu Gln Thr Ile Lys Gly Lys	
235 240 245	

Ile Val Ser Lys Gln Lys Leu Glu Leu Lys Thr Thr Glu Ala Gly Pro	250	255	260	265	
aga ttg atg tct gga aag cag gct gca gcc ata atc aaa gca gtt gat					929
Arg Leu Met Ser Gly Lys Gln Ala Ala Ala Ile Ile Lys Ala Val Asp	270		275	280	
tca aag tac acg gcc att ccc att gtg ggg cag gtc ttc cag agc cac					977
Ser Lys Tyr Thr Ala Ile Pro Ile Val Gly Gln Val Phe Gln Ser His	285		290	295	
tgt aaa gga tgt cct tct ctc tcg gag ctc tgg cgg tcc acc agg aaa					1025
Cys Lys Gly Cys Pro Ser Leu Ser Glu Leu Trp Arg Ser Thr Arg Lys	300		305	310	
tac ctg cag cct gac aac ctt tcc aag gct gag gct gtc aga aac ttc					1073
Tyr Leu Gln Pro Asp Asn Leu Ser Lys Ala Glu Ala Val Arg Asn Phe	315		320	325	
ctg gcc ttc att cag cac ctc agg act gcg aag aaa gaa gag atc ctt					1121
Leu Ala Phe Ile Gln His Leu Arg Thr Ala Lys Lys Glu Glu Ile Leu	330	335	340	345	
caa ata cta aag atg gaa aat aag gaa gta tta cct cag ctg gtg gat					1169
Gln Ile Leu Lys Met Glu Asn Lys Glu Val Leu Pro Gln Leu Val Asp	350		355	360	
gct gtc acc tct gct cag acc tca gac tca tta gaa gcc att ttg gac					1217
Ala Val Thr Ser Ala Gln Thr Ser Asp Ser Leu Glu Ala Ile Leu Asp	365		370	375	
ttt ttg gat ttc aaa agt gac agc agc att atc ctc cag gag agg ttt					1265
Phe Leu Asp Phe Lys Ser Asp Ser Ser Ile Ile Leu Gln Glu Arg Phe	380		385	390	
ctc tat gcc tgt gga ttt gct tct cat ccc aat gaa gaa ctc ctg aga					1313
Leu Tyr Ala Cys Gly Phe Ala Ser His Pro Asn Glu Glu Leu Leu Arg	395		400	405	
gcc ctc att agt aag ttc aaa ggt tct att ggt agc agt gac atc aga					1361
Ala Leu Ile Ser Lys Phe Lys Gly Ser Ile Gly Ser Ser Asp Ile Arg	410	415	420	425	
gaa act gtt atg atc atc act ggg aca ctt gtc aga aag ttg tgt cag					1409
Glu Thr Val Met Ile Ile Thr Gly Thr Leu Val Arg Lys Leu Cys Gln	430		435	440	
aat gaa ggc tgc aaa ctc aaa gca gta gtg gaa gct aag aag tta atc					1457
Asn Glu Gly Cys Lys Leu Lys Ala Val Val Glu Ala Lys Lys Leu Ile	445		450	455	
ctg gga gga ctt gaa aaa gca gag aaa aaa gag gac acc agg atg tat					1505
Leu Gly Gly Leu Glu Lys Ala Glu Lys Lys Glu Asp Thr Arg Met Tyr	460		465	470	

475	480	485	
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gct cac aat tat gac cgt ttc tcc agg agt gga tct tct tct gcc tac Ala His Asn Tyr Asp Arg Phe Ser Arg Ser Gly Ser Ser Ser Ala Tyr 605 610 615			1937
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gac att ctc tac tcg ggt tct ggc att cta agg aga agt aac ctg aac Asp Ile Leu Tyr Ser Gly Ser Gly Ile Leu Arg Arg Ser Asn Leu Asn 635 640 645			2033
atc ttt cag tac att ggg aag gct ggt ctt cac ggt agc cag gtg gtt Ile Phe Gln Tyr Ile Gly Lys Ala Gly Leu His Gly Ser Gln Val Val 650 655 660 665			2081
att gaa gcc caa gga ctg gaa gcc tta atc gca gcc acc cct gac gag Ile Glu Ala Gln Gly Leu Glu Ala Leu Ile Ala Ala Thr Pro Asp Glu 670 675 680			2129
ggg gag gag aac ctt gac tcc tat gct ggt atg tca gcc atc ctc ttt Gly Glu Glu Asn Leu Asp Ser Tyr Ala Gly Met Ser Ala Ile Leu Phe 685 690 695			2177
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Met Ser Lys Met Leu Ser Ala Ser Gly Asp Pro Ile Ser Val Val Lys	
715 720 725	
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Gly Leu Ile Leu Leu Ile Asp His Ser Gln Glu Leu Gln Leu Gln Ser	
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750 755 760	
tca ggt gca atg gag ttt agc ttg tgg tat cgt gag tct aaa acc cga	2417
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Val Lys Asn Arg Val Thr Val Val Ile Thr Thr Asp Ile Thr Val Asp	
780 785 790	
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gtt tgc atg cag atg gac aag gat gaa gct cca ttc agg caa ttt gag	2609
Val Cys Met Gln Met Asp Lys Asp Glu Ala Pro Phe Arg Gln Phe Glu	
830 835 840	
aaa aag tac gaa agg ctg tcc aca ggc aga ggt tat gtc tct cag aaa	2657
Lys Lys Tyr Glu Arg Leu Ser Thr Gly Arg Gly Tyr Val Ser Gln Lys	
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Arg Lys Glu Ser Val Leu Ala Gly Cys Glu Phe Pro Leu His Gln Glu	
860 865 870	
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Asn Ser Glu Met Cys Lys Val Val Phe Ala Pro Gln Pro Asp Ser Thr	
875 880 885	
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Ser Ser Gly Trp Phe	
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gaagggacaa ggcttttaaa agacttggtta gccaaacttca agaattaata tttatgtctc 3341
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140 145 150	
agc tta ttc cag atg cag cta agc tct gga act acc aac gag gta gat	531
Ser Leu Phe Gln Met Gln Leu Ser Ser Gly Thr Thr Asn Glu Val Asp	
155 160 165	
atc tct ggg gat tgt aaa gtg acc tac cag gcc caa caa gac aaa gtg	579
Ile Ser Gly Asp Cys Lys Val Thr Tyr Gln Ala Gln Gln Asp Lys Val	
170 175 180 185	
gtc aaa att aag gct ctg gat aca tgc aaa att gag cgg tct gga ttt	627
Val Lys Ile Lys Ala Leu Asp Thr Cys Lys Ile Glu Arg Ser Gly Phe	
190 195 200	
aca acg gca aac cag gtg ctg ggc gtc agt tca aaa gcc aca tct gtc	675
Thr Thr Ala Asn Gln Val Leu Gly Val Ser Ser Lys Ala Thr Ser Val	
205 210 215	
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Thr Thr Tyr Lys Ile Glu Asp Ser Phe Val Thr Ala Val Leu Ala Glu	
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gag acc agg gct ttt gcc ttg aac ttc caa caa acc ata gca gga aaa	771
Glu Thr Arg Ala Phe Ala Leu Asn Phe Gln Gln Thr Ile Ala Gly Lys	
235 240 245	
ata gtg tca aag cag aaa ttg gag ctg aag aca act gaa gcc ggc cca	819
Ile Val Ser Lys Gln Lys Leu Glu Leu Lys Thr Thr Glu Ala Gly Pro	
250 255 260 265	
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Arg Met Ile Pro Gly Lys Gln Val Ala Gly Val Ile Lys Ala Val Asp	
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Ser Lys Tyr Lys Ala Ile Pro Ile Val Gly Gln Val Leu Glu Arg Val	
285 290 295	
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Asn Leu Glu Pro Glu Asn Leu Ser Lys Ala Glu Ala Val Gln Ser Phe	
315 320 325	
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Leu Ala Phe Ile Gln His Leu Arg Thr Ser Arg Arg Glu Glu Ile Leu	
330 335 340 345	
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Glu Ile Leu Lys Ala Glu Lys Lys Glu Val Leu Pro Gln Leu Val Asp	

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Ala Val Thr Ser Ala Gln Thr Pro Asp Ser Leu Glu Ala Ile Leu Asp	
365 370 375	
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Phe Leu Asp Phe Lys Ser Asp Ser Ser Ile Ile Leu Gln Glu Arg Phe	
380 385 390	
ctc tat gcc tgt ggc ttt gcc acc cac cct gat gaa gaa ctc cta cga	1251
Leu Tyr Ala Cys Gly Phe Ala Thr His Pro Asp Glu Glu Leu Leu Arg	
395 400 405	
gcc ctc ctt agt aag ttc aaa ggt tcc ttt gca agc aac gac atc aga	1299
Ala Leu Leu Ser Lys Phe Lys Gly Ser Phe Ala Ser Asn Asp Ile Arg	
410 415 420 425	
gag tcg gtt atg atc atc att gga gcc cta gtc agg aag ctg tgt cag	1347
Glu Ser Val Met Ile Ile Ile Gly Ala Leu Val Arg Lys Leu Cys Gln	
430 435 440	
aat gaa ggc tgc aag ctc aag gca gtg gtg gaa gct aag aag ctg atc	1395
Asn Glu Gly Cys Lys Leu Lys Ala Val Val Glu Ala Lys Lys Leu Ile	
445 450 455	
ctg gga gga ctt gaa aaa cca gag aag aaa gaa gac acc aca atg tac	1443
Leu Gly Gly Leu Glu Lys Pro Glu Lys Lys Glu Asp Thr Thr Met Tyr	
460 465 470	
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475 480 485	
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490 495 500 505	
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510 515 520	
aag acc ttg aac agg ata tac cac cag aat cgt aag gtt cat gag aag	1635
Lys Thr Leu Asn Arg Ile Tyr His Gln Asn Arg Lys Val His Glu Lys	
525 530 535	
acg gtg cgc aca act gcc gct gct gtc atc tta aag aac cca tcc tac	1683
Thr Val Arg Thr Thr Ala Ala Ala Val Ile Leu Lys Asn Pro Ser Tyr	
540 545 550	
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Met Asp Val Lys Asn Ile Leu Leu Ser Ile Gly Glu Leu Pro Lys Glu	
555 560 565	
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Met Asn Lys Tyr Met Leu Thr Val Val Gln Asp Ile Leu His Phe Glu	
570 575 580 585	

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His	Asn	Tyr	Asp	Arg	Phe	Ser	Lys	Ser	Gly	Ser	Ser	Ser	Ala	Tyr	Thr		
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Gly	Tyr	Val	Glu	Arg	Ser	Pro		Ala	Ala	Ser	Thr	Tyr	Ser	Leu	Asp		
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atc	ctt	tac	tct	ggc	tct	ggc	att	ctg	agg	aga	agt	aac	ctg	aac	atc	1971	
Ile	Leu	Tyr	Ser	Gly	Ser	Gly	Ile	Leu	Arg	Arg	Ser	Asn	Leu	Asn	Ile		
	635					640					645						
ttc	cag	tac	atc	aaa	gga	aca	gag	ctt	cat	ggg	agt	cag	gtg	gtg	att	2019	
Phe	Gln	Tyr	Ile	Lys	Gly	Thr	Glu	Leu	His	Gly	Ser	Gln	Val	Val	Ile		
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tcc	aaa	atg	ctg	tcg	gca	tcc	ggc	gac	cct	gtc	agc	gtg	gtg	aaa	ggg	2211	
Ser	Lys	Met	Leu	Ser	Ala	Ser	Gly	Asp	Pro	Val	Ser	Val	Val	Lys	Gly		
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Leu	Ile	Leu	Leu	Ile	Asp	His	Ser	Gln	Asp	Ile	Gln	Leu	Gln	Ser	Gly		
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Gly	Ser	Met	Glu	Phe	Ser	Leu	Trp	Tyr	Arg	Glu	Ser	Lys	Thr	Arg	Val		
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Lys	Asn	Arg	Val	Ala	Val	Val	Ile	Thr	Ser	Asp	Val	Thr	Val	Asp	Ala		
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Ser	Phe	Val	Lys	Ala	Gly	Leu	Glu	Ser	Arg	Ala	Glu	Thr	Glu	Ala	Gly		
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Cys Met Gln Met Asp Lys Ala Glu Ala Pro Leu Arg Gln Phe Glu Thr				
830		835	840	
aag tat gaa agg cta tct aca ggc agg gga tat gtc tct cgg aga aga				2595
Lys Tyr Glu Arg Leu Ser Thr Gly Arg Gly Tyr Val Ser Arg Arg Arg				
845		850	855	
aaa gag agc cta gtg gcc gga tgt gaa ctc ccc ctc cat caa cag aac				2643
Lys Glu Ser Leu Val Ala Gly Cys Glu Leu Pro Leu His Gln Gln Asn				
860		865	870	
tct gag atg tgc aac gtg gta ttc cca cct cag cca gaa agc gat aac				2691
Ser Glu Met Cys Asn Val Val Phe Pro Pro Gln Pro Glu Ser Asp Asn				
875		880	885	
tcc ggt gga tgg ttt tga ttcccggtggg ttcccttcca ccagaacgat				2739
Ser Gly Gly Trp Phe				
890				
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